

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/912,951

1642

DATE: 06/04/98
TIME: 12:29:11

INPUT SET: S26385.raw

7 1/2

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information:
- 4
- 5 (i) APPLICANT: Cech, Thomas R.
- 6 Lingner, Joachim
- 7 Nakamura, Toru
- 8 Chapman, Karen B.
- 9 Morin, Gregg B.
- 10 Harley, Calvin
- 11 Andrews, William H.
- 12
- 13 (ii) TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
- 14 THERAPEUTIC METHODS
- 15
- 16 (iii) NUMBER OF SEQUENCES: 335
- 17
- 18 (iv) CORRESPONDENCE ADDRESS:
- 19 (A) ADDRESS: Townsend and Townsend and Crew LLP
- 20 (B) STREET: Two Embarcadero Center, 8th Floor
- 21 (C) CITY: San Francisco
- 22 (D) STATE: California
- 23 (E) COUNTRY: United States of America
- 24 (F) ZIP: 94111
- 25
- 26 (v) COMPUTER READABLE FORM:
- 27 (A) MEDIUM TYPE: Floppy disk
- 28 (B) COMPUTER: IBM PC compatible
- 29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 31
- 32 (vi) CURRENT APPLICATION DATA:
- 33 (A) APPLICATION NUMBER: US 08/912,951
- 34 (B) FILING DATE: 14-AUG-1997
- 35 (C) CLASSIFICATION:
- 36
- 37 (vii) PRIOR APPLICATION DATA:
- 38 (A) APPLICATION NUMBER: US 08/854,050
- 39 (B) FILING DATE: 09-MAY-1997
- 40 (C) CLASSIFICATION:
- 41
- 42 (vii) PRIOR APPLICATION DATA:
- 43 (A) APPLICATION NUMBER: US 08/851,843
- 44 (B) FILING DATE: 06-MAY-1997
- 45 (C) CLASSIFICATION:
- 46

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47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: US 08/846,017
49 (B) FILING DATE: 25-APR-1997
50 (C) CLASSIFICATION:
51
52 (vii) PRIOR APPLICATION DATA:
53 (A) APPLICATION NUMBER: US 08/844,419
54 (B) FILING DATE: 18-APR-1997
55 (C) CLASSIFICATION:
56
57 (vii) PRIOR APPLICATION DATA:
58 (A) APPLICATION NUMBER: US 08/724,643
59 (B) FILING DATE: 01-OCT-1996
60 (C) CLASSIFICATION:
61
62 (viii) ATTORNEY/AGENT INFORMATION:
63 (A) NAME: Apple, Randolph T.
64 (B) REGISTRATION NUMBER: 36,429
65 (C) REFERENCE/DOCKET NUMBER: 015389-002600US
66
67 (ix) TELECOMMUNICATION INFORMATION:
68 (A) TELEPHONE: (415) 576-0200
69 (B) TELEFAX: (415) 576-0300
70
71 (2) INFORMATION FOR SEQ ID NO:1:
72
73 (i) SEQUENCE CHARACTERISTICS:
74 (A) LENGTH: 4015 base pairs
75 (B) TYPE: nucleic acid
76 (C) STRANDEDNESS: single
77 (D) TOPOLOGY: linear
78
79 (ii) MOLECULE TYPE: cDNA
80
81
82 (ix) FEATURE:
83 (A) NAME/KEY: CDS
84 (B) LOCATION: 56..3454
85 (D) OTHER INFORMATION: /product= "hTRT"
86 /note= "human telomerase reverse
87 transcriptase (hTRT) catalytic protein
88 component"
89
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
92
93 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG 58
94 Met
95 1
96
97 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC 106
98 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
99 5 10 15

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100																		
101	TAC	CGC	GAG	GTG	CTG	CCG	CTG	GCC	ACG	TTC	GTG	CGG	CGC	CTG	GGG	CCC		154
102	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro		
103			20					25						30				
104																		
105	CAG	GGC	TGG	CGG	CTG	GTG	CAG	CGC	GGG	GAC	CCG	GCG	GCT	TTC	CGC	GCG		202
106	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala		
107		35					40					45						
108																		
109	CTG	GTG	GCC	CAG	TGC	CTG	GTG	TGC	GTG	CCC	TGG	GAC	GCA	CGG	CCG	CCC		250
110	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro		
111	50					55					60					65		
112																		
113	CCC	GCC	GCC	CCC	TCC	TTC	CGC	CAG	GTG	TCC	TGC	CTG	AAG	GAG	CTG	GTG		298
114	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val		
115					70					75					80			
116																		
117	GCC	CGA	GTG	CTG	CAG	AGG	CTG	TGC	GAG	CGC	GGC	GCG	AAG	AAC	GTG	CTG		346
118	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu		
119				85					90					95				
120																		
121	GCC	TTC	GGC	TTC	GCG	CTG	CTG	GAC	GGG	GCC	CGC	GGG	GGC	CCC	CCC	GAG		394
122	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu		
123			100					105					110					
124																		
125	GCC	TTC	ACC	ACC	AGC	GTG	CGC	AGC	TAC	CTG	CCC	AAC	ACG	GTG	ACC	GAC		442
126	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp		
127		115					120					125						
128																		
129	GCA	CTG	CGG	GGG	AGC	GGG	GCG	TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC		490
130	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly		
131	130					135					140					145		
132																		
133	GAC	GAC	GTG	CTG	GTT	CAC	CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG		538
134	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu		
135					150					155					160			
136																		
137	GTG	GCT	CCC	AGC	TGC	GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG		586
138	Val	Al																

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153	GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC	778
154	Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly	
155	230 235 240	
156		
157	GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC	826
158	Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala	
159	245 250 255	
160		
161	CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG	874
162	His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val	
163	260 265 270	
164		
165	TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG GGT GCG CTC	922
166	Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu	
167	275 280 285	
168		
169	TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC CAG CAC CAC GCG	970
170	Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala	
171	290 295 300 305	
172		
173	GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT	1018
174	Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys	
175	310 315 320	
176		
177	CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC	1066
178	Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp	
179	325 330 335	
180		
181	AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC	1114
182	Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser	
183	340 345 350	
184		
185	CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG	1162
186	Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg	
187	355 360 365	
188		
189	CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC	1210
190	Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg	
191	370 375 380 385	
192		
193	TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG	1258
194	Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala	
195	390 395 400	
196		
197	CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT	1306
198	Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala	
199	405 410 415	
200		
201	GCG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC	1354
202	Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly	
203	420 425 430	
204		
205	TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG	1402

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206	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
207		435					440					445					
208																	
209	CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
210	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
211	450					455					460					465	
212																	
213	CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
214	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
215					470					475					480		
216																	
217	CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
218	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
219				485					490					495			
220																	
221	GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
222	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
223			500					505					510				
224																	
225	GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
226	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
227		515					520					525					
228																	
229	CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
230	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
231	530					535					540					545	
232																	
233	CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
234	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
235					550					555					560		
236																	
237	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
238	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
239				565					570					575			
240																	
241	AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
242	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
243			580					585					590				
244																	
245	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
246	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
247		595					600					605					
248																	
249	CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
250	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
251	610					615					620					625	
252																	
253	AAG	CCT	GAC	GGG	CTG	CGG	CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	1978
254	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	
255					630					635					640		
256																	
257	GCC	AGA	ACG	TTC	CGC	AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	2026
258	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	

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